

InterPro: IP001643; Caliciviridae.
 ID PF00915; Caliciviridae.
 FT MON_TER 1 1
 SO SEQUENCE 114 AA; 11222 MW; 1F10967005HBAA5 CDS64;

Query Match
 Best Local Similarity 76.0%; Score 48; DB 12; Length 114;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSAAVATYSP 10
 DB 51 PSAAVATYSP 60

RESULT 6
 ID 041241 PRELIMINARY; PRT: 114 AA.

AC 041241:
 DT 01-JAN-1998 (TREMBLREL: 05, Created)
 DT 01-JAN-1998 (TREMBLREL: 05, Last sequence update)
 DT 01-JUN-2001 (TREMBLREL: 17, Last annotation update)
 DE CAPSID PROTEIN (FRAGMENT).
 OS Rabbit hemorrhagic disease virus (RHDV).
 CC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 CC Lagovirus.
 CX NCBI_TaxID: 11976;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPAIN 95C;
 RX MEDLINE:9714153; PubMed:9170495;
 RA Novotny N., Baschana C.R., Ballejo-Jordany A., Gavier-Widen D.,
 Uhlen M., Belak S.;
 RA "Phylogenetic analysis of rabbit haemorrhagic disease and European
 RT brown hare syndrome viruses by comparison of sequences from the capsid
 RT protein gene.";
 RL Arch. Virol. 142:657-673(1997).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPAIN 95C;
 RX Ros C.;
 RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: 065349; AAF62794.1;
 DR InterPro: IP001643; Caliciviridae.
 DR Pfam: PF00915; Caliciviridae.
 FT MON_TER 1 1
 FT NON_TER 114 114
 SO SEQUENCE 114 AA; 11220 MW; 2925H02965B098A1 CDS64;

Query Match
 Best Local Similarity 76.0%; Score 48; DB 12; Length 114;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSAAVATYSP 10
 DB 51 PSAAVATYSP 60

RESULT 7
 ID 041241 PRELIMINARY; PRT: 159 AA.

AC 041241:
 DT 01-MAY-1999 (TREMBLREL: 10, Created)
 DT 01-MAY-1999 (TREMBLREL: 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLREL: 17, Last annotation update)
 DE ORF-2.
 OS porcine coronavirus type 2-G.
 CC Viruses; ssDNA viruses; Citroviridae; Citrovirus.
 CX NCBI_TaxID: 85543;
 RN 11
 RP SEQUENCE FROM N.A.

Ramel A.L., Navar C.P.S.;
 RT "Nucleotide sequence of four different isolates of citrovirus detected
 RT in pigs with various clinical syndromes.";
 RL Submitted (Nov 1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF109308; AAO0462.1;
 DR InterPro: IP004383; Citroviridae.
 DR Pfam: PF02443; Citroviridae.
 SO SEQUENCE 159 AA; 19906 MW; E45771A25B5600B CDS64;

Query Match
 Best Local Similarity 76.0%; Score 48; DB 12; Length 159;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 PSAAVATYSP 10
 DB 141 PSAAVATYSP 140

RESULT 8
 ID 041242 PRELIMINARY; PRT: 243 AA.

AC 041242:
 DT 01-OCT-2000 (TREMBLREL: 15, Created)
 DT 01-OCT-2000 (TREMBLREL: 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLREL: 17, Last annotation update)
 DE PUTATIVE CAPSID PROTEIN.
 OS CAP.
 CC Porcine coronavirus type 2.
 CC Viruses; ssDNA viruses; Citroviridae; Citrovirus.
 CX NCBI_TaxID: 85708;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-26607;
 RX MEDLINE:20341547; PubMed:10878042;
 RA Penau M., Balbar P.G., Gill M., Toth T.E., Meng X.L.;
 RA "Genomic characterization of type 2 porcine coronavirus (PVC-2) from
 RT pigs with PMS in different geographic regions of North America and
 RT development of a differential PCR-RFLP assay to detect and
 RT differentiate infections between PVC-1 and PVC-2.";
 RL J. Clin. Microbiol. 38:2494-2503(2000).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN-26607;
 RX Penau M., Balbar P.G., Gill M., Toth T.E., Meng X.L.;
 RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF244039; AAF87229.1;
 DR InterPro: IP004383; Citroviridae.
 DR Pfam: PF02443; Citroviridae.
 SO SEQUENCE 243 AA; 27965 MW; 1AB2D812871E76F4 CDS64;

Query Match
 Best Local Similarity 76.0%; Score 48; DB 12; Length 243;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 PSAAVATYSP 10
 DB 141 PSAAVATYSP 140

RESULT 9
 ID 041243 PRELIMINARY; PRT: 279 AA.

AC 041243:
 DT 01-OCT-2000 (TREMBLREL: 15, Created)
 DT 01-OCT-2000 (TREMBLREL: 15, Last sequence update)
 DT 01-MAY-2001 (TREMBLREL: 16, Last annotation update)
 DE HYPOTHETICAL_29.3 KDA PROTEIN.
 OS L5075-02.
 CC Lactobacillus malorum.
 CC Eukaryota; Kinetoplastida; Trypanosomatidae; Trichomonas.
 CX NCBI_TaxID: 5664;

PN	111
PP	SEQUENCE FROM N.A.
RK	SIBAIN FRIEDLINE
RA	Bock A., Klages S., Rothardt K., Frons A.C., Graft M.,
RE	Korandrom M.A., Barrell B.G., To the EMBL/Genbank/Joint databases
RL	Submitted (Apr. 2000) to the EMBL/Genbank/Joint databases
RN	[2]
RP	SEQUENCE FROM N.A.
RQ	SIBAIN FRIEDLINE
RX	MEDLINE 9814447; PubMed 947741;
SA	Frons A.C., Lewis S.M., Korandrom M., Zhang L., Chan H.M.,
SB	Smith D.F.;
SC	"A physical map of the Eichmannia mori protein genome";
SD	Genome Res. 6:145-149(1998).
SE	EMBL: AF145522; CABIOS:4.1;
SF	Hybrid local protein.
SG	SEQUENCE 276 AA; 29435 MW; 591018DALtons etc etc etc;
SH	
SI	Index Match
SJ	Best Local Similarity: 80.0%; Prod. No.: 16;
SK	Method: E; Compensation: 0; Mismatches: 2; Indels: 0; Gaps:
SL	
SM	I PSAAALVSP: 10
SN	IIIII I I
SO	142 PSAAALVSP: 141
SP	
SQ	REFID: 19
SR	CDB124
SS	GME124 PRELIMINARY: PRG: 5/9 AA.
ST	GME124
TU	01 NOV 1996 (EHEHREL 01, created)
TV	01 NOV 1996 (EHEHREL 01, last sequence update)
TX	01 NOV 2001 (EHEHREL 17, last annotation update)
TY	V001.
TA	Rabbit hemorrhagic disease virus (RHV).
TB	Virus: SSRNA positive strand viruses; no DNA stage; Valtoviridae;
TC	Lacovirus.
TD	NR01 TORO 11976;
TE	111
TF	SEQUENCE FROM N.A.
TG	SIBAIN AST/89;
TH	MEDLINE 94358742; PubMed 9077041;
TI	Bock J., Castis R., Martin M., Martin Alonso J., Curranes R.,
TJ	Pinto M., Parra F.;
TK	"Molecular cloning, sequencing and expression in Escherichia coli of
TL	the capsid protein gene from rabbit haemorrhagic disease virus
TM	(Spanish isolate AST/89)".
TO	J. Gen. Virol. 75:2409-2414(1994);
TP	121
TQ	SEQUENCE FROM N.A.
TR	SIBAIN AST/89;
TS	MEDLINE 94070565; PubMed 144146;
TT	Bock J., Martin M., Castis R., Pinto M., Parra F.;
TU	"In vitro translation of a subgenomic mRNA from purified virions of
TV	the Spanish field isolate AST/89 of rabbit hemorrhagic disease virus
TX	(RHV)".
TY	Virus Res. 26:33-40(1992);
TA	141
TB	SEQUENCE OF 142 FROM N.A.
TC	SIBAIN AST/89;
TD	MEDLINE 9425896; PubMed 9406721;
TE	Parra F., Bock J.A., Martin M.S., Castis R.;
TF	"The amino terminal sequence of VP60 from rabbit hemorrhagic disease
TF	virus supports its putative subgenomic activity".
TF	Virus Res. 27:219-228(1993);
TF	141
TF	SEQUENCE FROM N.A.
TF	SIBAIN AST/89;
TF	Parra F.;
TF	Submitted (Jul. 1994) to the EMBL/Genbank/Joint databases.
TF	EMBL: Z44572; CABIOS:4.1;

Query Match	76.0%	Score 48	DB 12	Length 979
Host Local Similarity	70.0%	Prod. No. 45		
Matches	72	Conservative	4	Mismatches 1; Indels 0; Gaps 0
01	1	PSANVAL115P	10	
02	1	11111111		
03	4.29	PSANVAL11P	438	
RESULT 12				
04	1	096124		
05	096124	PR11MINARY		PR12 69% AA.
06	01 NOV-1996 (11EMB101.01, Created)			
07	01 NOV-1996 (11EMB101.01, Last sequence update)			
08	01 JUN-2001 (11EMB101.17, Last annotation update)			
09	01 JUN-2001 (11EMB101.17, Last annotation update)			
10	01 JUN-2001 (11EMB101.17, Last annotation update)			
11	01 JUN-2001 (11EMB101.17, Last annotation update)			
12	01 JUN-2001 (11EMB101.17, Last annotation update)			
13	01 JUN-2001 (11EMB101.17, Last annotation update)			
14	01 JUN-2001 (11EMB101.17, Last annotation update)			
15	01 JUN-2001 (11EMB101.17, Last annotation update)			
16	01 JUN-2001 (11EMB101.17, Last annotation update)			
17	01 JUN-2001 (11EMB101.17, Last annotation update)			
18	01 JUN-2001 (11EMB101.17, Last annotation update)			
19	01 JUN-2001 (11EMB101.17, Last annotation update)			
20	01 JUN-2001 (11EMB101.17, Last annotation update)			
21	01 JUN-2001 (11EMB101.17, Last annotation update)			
22	01 JUN-2001 (11EMB101.17, Last annotation update)			
23	01 JUN-2001 (11EMB101.17, Last annotation update)			
24	01 JUN-2001 (11EMB101.17, Last annotation update)			
25	01 JUN-2001 (11EMB101.17, Last annotation update)			
26	01 JUN-2001 (11EMB101.17, Last annotation update)			
27	01 JUN-2001 (11EMB101.17, Last annotation update)			
28	01 JUN-2001 (11EMB101.17, Last annotation update)			
29	01 JUN-2001 (11EMB101.17, Last annotation update)			
30	01 JUN-2001 (11EMB101.17, Last annotation update)			
31	01 JUN-2001 (11EMB101.17, Last annotation update)			
32	01 JUN-2001 (11EMB101.17, Last annotation update)			
33	01 JUN-2001 (11EMB101.17, Last annotation update)			
34	01 JUN-2001 (11EMB101.17, Last annotation update)			
35	01 JUN-2001 (11EMB101.17, Last annotation update)			
36	01 JUN-2001 (11EMB101.17, Last annotation update)			
37	01 JUN-2001 (11EMB101.17, Last annotation update)			
38	01 JUN-2001 (11EMB101.17, Last annotation update)			
39	01 JUN-2001 (11EMB101.17, Last annotation update)			
40	01 JUN-2001 (11EMB101.17, Last annotation update)			
41	01 JUN-2001 (11EMB101.17, Last annotation update)			
42	01 JUN-2001 (11EMB101.17, Last annotation update)			
43	01 JUN-2001 (11EMB101.17, Last annotation update)			
44	01 JUN-2001 (11EMB101.17, Last annotation update)			
45	01 JUN-2001 (11EMB101.17, Last annotation update)			
46	01 JUN-2001 (11EMB101.17, Last annotation update)			
47	01 JUN-2001 (11EMB101.17, Last annotation update)			
48	01 JUN-2001 (11EMB101.17, Last annotation update)			
49	01 JUN-2001 (11EMB101.17, Last annotation update)			
50	01 JUN-2001 (11EMB101.17, Last annotation update)			
51	01 JUN-2001 (11EMB101.17, Last annotation update)			
52	01 JUN-2001 (11EMB101.17, Last annotation update)			
53	01 JUN-2001 (11EMB101.17, Last annotation update)			
54	01 JUN-2001 (11EMB101.17, Last annotation update)			
55	01 JUN-2001 (11EMB101.17, Last annotation update)			
56	01 JUN-2001 (11EMB101.17, Last annotation update)			
57	01 JUN-2001 (11EMB101.17, Last annotation update)			
58	01 JUN-2001 (11EMB101.17, Last annotation update)			
59	01 JUN-2001 (11EMB101.17, Last annotation update)			
60	01 JUN-2001 (11EMB101.17, Last annotation update)			
61	01 JUN-2001 (11EMB101.17, Last annotation update)			
62	01 JUN-2001 (11EMB101.17, Last annotation update)			
63	01 JUN-2001 (11EMB101.17, Last annotation update)			
64	01 JUN-2001 (11EMB101.17, Last annotation update)			
65	01 JUN-2001 (11EMB101.17, Last annotation update)			
66	01 JUN-2001 (11EMB101.17, Last annotation update)			
67	01 JUN-2001 (11EMB101.17, Last annotation update)			
68	01 JUN-2001 (11EMB101.17, Last annotation update)			
69	01 JUN-2001 (11EMB101.17, Last annotation update)			
70	01 JUN-2001 (11EMB101.17, Last annotation update)			
71	01 JUN-2001 (11EMB101.17, Last annotation update)			
72	01 JUN-2001 (11EMB101.17, Last annotation update)			
73	01 JUN-2001 (11EMB101.17, Last annotation update)			
74	01 JUN-2001 (11EMB101.17, Last annotation update)			
75	01 JUN-2001 (11EMB101.17, Last annotation update)			
76	01 JUN-2001 (11EMB101.17, Last annotation update)			
77				

SEQUENCE FROM N.A.
 AC STRAIN AST/89;
 RX MEDLINE=93070565; PubMed 1441746;
 RA Bosa J., Martin M., Casals R., Pileto M., Parra F.;
 RT "In vitro translation of a subgenomic mRNA from purified variants of
 RT the Spanish field isolate AST/89 of rabbit hemorrhagic disease virus
 RT (RHDV).";
 RL Virus Res. 26:33-40(1992)
 RN [3]
 RP SEQUENCE OF 1-149 FROM N.A.
 RC STRAIN-AST/89;
 RX MEDLINE=93255896; PubMed 8488721;
 RA Parra F., Bosa J.A., Martin M.S., Casals R.;
 RT "The amino terminal sequence of VP60 from rabbit hemorrhagic disease
 RT virus supports its putative subgenomic origin.";
 RL Virus Res. 27:219-228(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AST/89;
 RA Parra F.;
 RT Submitted (JUL-1993) to the EMBL/GenBank/DBJ databases.
 RX EMBL: Z24757; CAAB0881.1;
 RT InterPro: IPR001643; Caliciviridae.
 RA Pfam: PF00915; Caliciviridae; 1.
 DR PRINTS: PR00918; CALICIVIRUSNS.
 FT N-TER 1
 SEQUENCE 695 AA: 73731 MW: 620921628969898A Cleaved;
 Query Match 76.0% Score 48; DB 12; Length 695;
 Best Local Similarity 70.0%; Pred. No. 45;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 13
 ID 086117 PRELIMINARY; PRT: 244 AA.
 AC 086117;
 DT 01-NOV-1996 (TREMURIEL 01, created)
 DT 01-NOV-1996 (TREMURIEL 01, last sequence update)
 DT 01-JUN-2001 (TREMURIEL 17, last annotation update)
 DE (SD).
 OS Rabbit hemorrhagic disease virus (RHDV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 CC Lagovirus.
 NCBI_TaxID=11976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SD;
 RX MEDLINE=95250304; PubMed-7732658;
 RA Rasmussen D., Huguet S., Madelaine M.F., Vautherot J.F.;
 RT "Sequence and genomic organization of a rabbit hemorrhagic disease
 RT virus isolated from a wild rabbit.";
 RL Virus Genes 9:121-132(1995).
 DR EMBL: Z29514; CAAB2635.1;
 DR InterPro: IPR000317; Endoplasmic_C24.
 DR InterPro: IPR000605; RNA_polase.
 DR InterPro: IPR001205; RNA_polase.
 DR InterPro: IPR001643; Caliciviridae.
 DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
 DR Pfam: PF00915; Caliciviridae; 1.
 DR PRINTS: PR00918; CALICIVIRUSNS.
 DR PRINTS: PR00918; CALICIVIRUSNS.
 SO SEQUENCE 244 AA: 257120 MW: 1940134473588777 Cleaved;
 Query Match 76.0% Score 48; DB 12; Length 244;
 Best Local Similarity 70.0%; Pred. No. 15;02;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 14
 ID 086117 PRELIMINARY; PRT: 244 AA.
 AC 086117;
 DT 01-NOV-1996 (TREMURIEL 01, created)
 DT 01-NOV-1996 (TREMURIEL 01, last sequence update)
 DT 01-JUN-2001 (TREMURIEL 17, last annotation update)
 DE Polypeptide.
 OS Rabbit hemorrhagic disease virus (RHDV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 CC Lagovirus.
 NCBI_TaxID=11976;
 RN [1]
 RP SEQUENCE OF 1449 244 FROM N.A.
 RC STRAIN-AST/89;
 RX MEDLINE=94358742; PubMed 8077941;
 RA Bosa J., Casals R., Martin M., Martin Alonso J., Dominguez R.,
 RA Pileto M., Parra F.;
 RT "Molecular cloning, sequencing and expression in Escherichia coli of
 RT the capsid protein gene from rabbit hemorrhagic disease virus
 RT (Spanish isolate AST/89).";
 RL J. Gen. Virol. 75:2409-2413(1994).
 RN [2]
 RP SEQUENCE OF 1649-1796 FROM N.A.
 RC STRAIN-AST/89;
 RX MEDLINE=94358996; PubMed 8488721;
 RA Parra F., Bosa J.A., Martin M.S., Casals R.;
 RT "The amino terminal sequence of VP60 from rabbit hemorrhagic disease
 RT virus supports its putative subgenomic origin.";
 RL Virus Res. 27:219-228(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AST/89;
 RA Casals R., Martin Alonso J., Bosa J., Parra F.;
 RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RX EMBL: Z49271; CAAB9265.1;
 RT InterPro: IPR00317; Endoplasmic_C24.
 DR InterPro: IPR00605; RNA_polase.
 DR InterPro: IPR001205; RNA_polase.
 DR InterPro: IPR001643; Caliciviridae.
 DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
 DR Pfam: PF00915; Caliciviridae; 1.
 DR PRINTS: PR00918; CALICIVIRUSNS.
 DR PRINTS: PR00918; CALICIVIRUSNS.
 KM Polypeptide.
 SO SEQUENCE 244 AA: 256769 MW: 92646096644994A Cleaved;
 Query Match 76.0% Score 48; DB 12; Length 244;
 Best Local Similarity 70.0%; Pred. No. 15;02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 15
 ID 09ANK2 PRELIMINARY; PRT: 534 AA.
 AC 09ANK2;
 DT 01-JUN-2001 (TREMURIEL 17, created)
 DT 01-JUN-2001 (TREMURIEL 17, last sequence update)
 DT 01-JUN-2001 (TREMURIEL 17, last annotation update)

